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SEQUENCE LISTING

<110> DING, Jeak Ling
HO, Bow

<120> Sushi Peptide Multimer

<130> 79612-60

<140> CA2432972

<141> 2003-07-04

<160> 9

<170> PatentIn Ver. 2.0

<210> 1

<211> 34

<212> PRT

<213> Artificial Sequence

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<223> Sushi-3 peptide

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Phe Pro Gln Gly Thr Glu Val Thr Tyr Thr Cys Ser Gly Asn Tyr Phe
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Leu Met

<210> 2

<211> 34

<212> PRT

<213> Artificial Sequence

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<223> Sushi-3delta peptide

<400> 2

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Phe Pro Gln Gly Thr Glu Val Thr Tyr Thr Cys Ser Gly Asn Tyr Phe
20 25 30

Leu Met

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<210> 3
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 <212> DNA
 <213> Artificial Sequence

<220>
 <223> forward primer

<400> 3

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 <223> reverse primer

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 <213> Carcinoscorpius rotundicauda

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 1 5 10

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 Val Leu Gly Leu Leu Ala Gln Lys Met Arg Pro Val Gln Ser Lys Gly
 15 20 25

gta gat cta ggc ttg tgt gat gaa acg agg ttc gag tgt aag tgt ggc 146
 Val Asp Leu Gly Leu Cys Asp Glu Thr Arg Phe Glu Cys Lys Cys Gly
 30 35 40

gat cca ggc tat gtg ttc aac att cca gtg aaa caa tgt aca tac ttt 194
 Asp Pro Gly Tyr Val Phe Asn Ile Pro Val Lys Gln Cys Thr Tyr Phe
 45 50 55

tat cga tgg agg ccg tat tgt aaa cca tgt gat gac ctg gag gct aag 242
 Tyr Arg Trp Arg Pro Tyr Cys Lys Pro Cys Asp Asp Leu Glu Ala Lys
 60 65 70 75

gat att tgt cca aag tac aaa cga tgt caa gag tgt aag gct ggt ctt 290
 Asp Ile Cys Pro Lys Tyr Lys Arg Cys Gln Glu Cys Lys Ala Gly Leu
 80 85 90

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gat agt tgt gtt act tgt cca cct aac aaa tat ggt act tgg tgt agc	338
Asp Ser Cys Val Thr Cys Pro Pro Asn Lys Tyr Gly Thr Trp Cys Ser	
95 100 105	
ggt gaa tgt cag tgt aag aat gga ggt atc tgt gac cag agg aca gga	386
Gly Glu Cys Gln Cys Lys Asn Gly Gly Ile Cys Asp Gln Arg Thr Gly	
110 115 120	
gct tgt gca tgt cgt gac aga tat gaa ggg gtg cac tgt gaa att ctc	434
Ala Cys Ala Cys Arg Asp Arg Tyr Glu Gly Val His Cys Glu Ile Leu	
125 130 135	
aaa ggt tgt cct ctt ctt cca tcg gat tct cag gtt cag gaa gtc aga	482
Lys Gly Cys Pro Leu Leu Pro Ser Asp Ser Gln Val Gln Glu Val Arg	
140 145 150 155	
aat cca cca gat aat ccc caa act att gac tac agc tgt tca cca ggg	530
Asn Pro Pro Asp Asn Pro Gln Thr Ile Asp Tyr Ser Cys Ser Pro Gly	
160 165 170	
ttc aag ctt aag ggt atg gca cga att agc tgt ctc cca aat gga cag	578
Phe Lys Leu Lys Gly Met Ala Arg Ile Ser Cys Leu Pro Asn Gly Gln	
175 180 185	
tgg agt aac ttt cca ccc aaa tgt att cga gaa tgt gcc atg gtt tca	626
Trp Ser Asn Phe Pro Pro Lys Cys Ile Arg Glu Cys Ala Met Val Ser	
190 195 200	
tct cca gaa cat ggg aaa gtg aat gct ctt agt ggt gat atg ata gaa	674
Ser Pro Glu His Gly Lys Val Asn Ala Leu Ser Gly Asp Met Ile Glu	
205 210 215	
ggg gct act tta cgg ttc tca tgt gat agt ccc tac tac ttg att ggt	722
Gly Ala Thr Leu Arg Phe Ser Cys Asp Ser Pro Tyr Tyr Leu Ile Gly	
220 225 230 235	
caa gaa aca tta acc tgt cag ggt aat ggt cag tgg aat gga cag ata	770
Gln Glu Thr Leu Thr Cys Gln Gly Asn Gly Gln Trp Asn Gly Gln Ile	
240 245 250	
cca caa tgt aag aac ttg gtc ttc tgt cct gac ctg gat cct gta aac	818
Pro Gln Cys Lys Asn Leu Val Phe Cys Pro Asp Leu Asp Pro Val Asn	
255 260 265	
cat gct gaa cac aag gtt aaa att ggt gtg gaa caa aaa tat ggt cag	866
His Ala Glu His Lys Val Lys Ile Gly Val Glu Gln Lys Tyr Gly Gln	
270 275 280	
ttt cct caa ggc act gaa gtg acc tat acg tgt tcg ggt aac tac ttc	914
Phe Pro Gln Gly Thr Glu Val Thr Tyr Thr Cys Ser Gly Asn Tyr Phe	
285 290 295	
ttg atg ggt ttt gac acc tta aaa tgt aac cct gat ggg tct tgg tca	962
Leu Met Gly Phe Asp Thr Leu Lys Cys Asn Pro Asp Gly Ser Trp Ser	
300 305 310 315	
gga tca cag cca tcc tgt gtt aaa gtg gca gac aga gag gtc gac tgt	1010
Gly Ser Gln Pro Ser Cys Val Lys Val Ala Asp Arg Glu Val Asp Cys	
320 325 330	

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gac agt aaa gct gta gac ttc ttg gat gat gtt ggt gaa cct gtc agg	1058
Asp Ser Lys Ala Val Asp Phe Leu Asp Asp Val Gly Glu Pro Val Arg	
335 340 345	
atc cac tgt cct gct ggc tgt tct ttg aca gct ggt act gtg tgg ggt	1106
Ile His Cys Pro Ala Gly Cys Ser Leu Thr Ala Gly Thr Val Trp Gly	
350 355 360	
aca gcc ata tac cat gaa ctt tcc tca gtg tgt cgt gca gcc atc cat	1154
Thr Ala Ile Tyr His Glu Leu Ser Ser Val Cys Arg Ala Ala Ile His	
365 370 375	
gct ggc aag ctt cca aac tct gga gga gcg gtg cat gtt gtg aac aat	1202
Ala Gly Lys Leu Pro Asn Ser Gly Gly Ala Val His Val Val Asn Asn	
380 385 390 395	
ggc ccc tac tcg gac ttt ctg ggt agt gac ctg aat ggg ata aaa tcg	1250
Gly Pro Tyr Ser Asp Phe Leu Gly Ser Asp Leu Asn Gly Ile Lys Ser	
400 405 410	
gaa gag ttg aag tct ctt gcc cgg agt ttc cga ttc gat tat gtc cgt	1298
Glu Glu Leu Lys Ser Leu Ala Arg Ser Phe Arg Phe Asp Tyr Val Arg	
415 420 425	
tcc tcc aca gca ggt aaa tca gga tgt cct gat gga tgg ttt gag gta	1346
Ser Ser Thr Ala Gly Lys Ser Gly Cys Pro Asp Gly Trp Phe Glu Val	
430 435 440	
gac gag aac tgt gtg tac gtt aca tca aaa cag aga gcc tgg gaa aga	1394
Asp Glu Asn Cys Val Tyr Val Thr Ser Lys Gln Arg Ala Trp Glu Arg	
445 450 455	
gct caa ggt gtg tgt acc aat atg gct gct cgt ctt gct gtg ctg gac	1442
Ala Gln Gly Val Cys Thr Asn Met Ala Ala Arg Leu Ala Val Leu Asp	
460 465 470 475	
aaa gat gta att cca aat tcg ttg act gag act cta cga ggg aaa ggg	1490
Lys Asp Val Ile Pro Asn Ser Leu Thr Glu Thr Leu Arg Gly Lys Gly	
480 485 490	
tta aca acc acg tgg ata gga ttg cac aga cta gat gct gag aag ccc	1538
Leu Thr Thr Thr Trp Ile Gly Leu His Arg Leu Asp Ala Glu Lys Pro	
495 500 505	
ttt att tgg gag tta atg gat cgt agt aat gtg gtt ctg aat gat aac	1586
Phe Ile Trp Glu Leu Met Asp Arg Ser Asn Val Val Leu Asn Asp Asn	
510 515 520	

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cta aca ttc tgg gcc tct ggc gaa cct gga aat gaa act aac tgt gta	1634
Leu Thr Phe Trp Ala Ser Gly Glu Pro Gly Asn Glu Thr Asn Cys Val	
525 530 535	
tat atg gac atc caa gat cag ttg cag tct gtg tgg aaa acc aag tca	1682
Tyr Met Asp Ile Gln Asp Gln Leu Gln Ser Val Trp Lys Thr Lys Ser	
540 545 550 555	
tgt ttt cag ccc tca agt ttt gct tgc atg atg gat ctg tca gac aga	1730
Cys Phe Gln Pro Ser Ser Phe Ala Cys Met Met Asp Leu Ser Asp Arg	
560 565 570	
aat aaa gcc aaa tgc gat gat cct gga tca ctg gaa aat gga cac gcc	1778
Asn Lys Ala Lys Cys Asp Asp Pro Gly Ser Leu Glu Asn Gly His Ala	
575 580 585	
aca ctt cat gga caa agt att gat ggg ttc tat gct ggt tct tct ata	1826
Thr Leu His Gly Gln Ser Ile Asp Gly Phe Tyr Ala Gly Ser Ser Ile	
590 595 600	
agg tac agc tgt gag gtt ctc cac tac ctc agt gga act gaa acc gta	1874
Arg Tyr Ser Cys Glu Val Leu His Tyr Leu Ser Gly Thr Glu Thr Val	
605 610 615	
act tgt aca aca aat ggc aca tgg agt gct cct aaa cct cga tgt atc	1922
Thr Cys Thr Thr Asn Gly Thr Trp Ser Ala Pro Lys Pro Arg Cys Ile	
620 625 630 635	
aaa gtc atc acc tgc caa aac ccc cct gta cca tca tat ggt tct gtg	1970
Lys Val Ile Thr Cys Gln Asn Pro Pro Val Pro Ser Tyr Gly Ser Val	
640 645 650	
gaa atc aaa ccc cca agt cgg aca aac tcg ata agt cgt gtt ggg tca	2018
Glu Ile Lys Pro Pro Ser Arg Thr Asn Ser Ile Ser Arg Val Gly Ser	
655 660 665	
cct ttc ttg agg ttg cca cgg tta ccc ctc cca tta gct aga gca gcc	2066
Pro Phe Leu Arg Leu Pro Arg Leu Pro Leu Pro Leu Ala Arg Ala Ala	
670 675 680	
aaa cct cct cca aaa cct aga tcc tca caa ccc tct act gtg gac ttg	2114
Lys Pro Pro Pro Lys Pro Arg Ser Ser Gln Pro Ser Thr Val Asp Leu	
685 690 695	
gct tct aaa gtt aaa cta cct gaa ggt cat tac cgg gta ggg tct cga	2162
Ala Ser Lys Val Lys Leu Pro Glu Gly His Tyr Arg Val Gly Ser Arg	
700 705 710 715	
gcc atc tac acg tgc gag tcg aga tac tac gaa cta ctt gga tct caa	2210
Ala Ile Tyr Thr Cys Glu Ser Arg Tyr Tyr Glu Leu Leu Gly Ser Gln	
720 725 730	
ggc aga aga tgt gac tct aat gga aac tgg agt ggt cgg cca gcg agc	2258
Gly Arg Arg Cys Asp Ser Asn Gly Asn Trp Ser Gly Arg Pro Ala Ser	
735 740 745	

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tgt att cca gtt tgt gga cgg tca gac tct cct cgt tct cct ttt atc	2306
Cys Ile Pro Val Cys Gly Arg Ser Asp Ser Pro Arg Ser Pro Phe Ile	
750 755 760	
tgg aat ggg aat tct aca gaa ata ggt cag tgg ccg tgg cag gca gga	2354
Trp Asn Gly Asn Ser Thr Glu Ile Gly Gln Trp Pro Trp Gln Ala Gly	
765 770 775	
atc tct aga tgg ctt gca gac cac aat atg tgg ttt ctc cag tgt gga	2402
Ile Ser Arg Trp Leu Ala Asp His Asn Met Trp Phe Leu Gln Cys Gly	
780 785 790 795	
gga tct cta ttg aat gag aaa tgg atc gtc act gct gcc cac tgt gtc	2450
Gly Ser Leu Leu Asn Glu Lys Trp Ile Val Thr Ala Ala His Cys Val	
800 805 810	
acc tac tct gct act gct gag att att gac ccc aat cag ttt aaa atg	2498
Thr Tyr Ser Ala Thr Ala Glu Ile Ile Asp Pro Asn Gln Phe Lys Met	
815 820 825	
tat ctg ggc aag tac tac cgt gat gac agt aga gac gat gac tat gta	2546
Tyr Leu Gly Lys Tyr Tyr Arg Asp Asp Ser Arg Asp Asp Tyr Val	
830 835 840	
caa gta aga gag gct ctt gag atc cac gtg aat cct aac tac gac ccc	2594
Gln Val Arg Glu Ala Leu Glu Ile His Val Asn Pro Asn Tyr Asp Pro	
845 850 855	
ggc aat ctc aac ttt gac ata gcc cta att caa ctg aaa act cct gtt	2642
Gly Asn Leu Asn Phe Asp Ile Ala Leu Ile Gln Leu Lys Thr Pro Val	
860 865 870 875	
act ttg aca aca cga gtc caa cca atc tgt ctg cct act gac atc aca	2690
Thr Leu Thr Thr Arg Val Gln Pro Ile Cys Leu Pro Thr Asp Ile Thr	
880 885 890	
aca aga gaa cac ttg aag gag gga aca tta gca gtg gtg aca ggt tgg	2738
Thr Arg Glu His Leu Lys Glu Gly Thr Leu Ala Val Val Thr Gly Trp	
895 900 905	
ggg ttg aat gaa aac aac acc tat tca gag acg att caa caa gct gtg	2786
Gly Leu Asn Glu Asn Asn Thr Tyr Ser Glu Thr Ile Gln Gln Ala Val	
910 915 920	
cta cct gtt gtt gca gcc agc acc tgt gaa gag ggg tac aag gaa gca	2834
Leu Pro Val Val Ala Ala Ser Thr Cys Glu Glu Gly Tyr Lys Glu Ala	
925 930 935	
gac tta cca ctg aca gta aca gag aac atg ttc tgt gca ggt tac aag	2882
Asp Leu Pro Leu Thr Val Thr Glu Asn Met Phe Cys Ala Gly Tyr Lys	
940 945 950 955	
aag gga cgt tat gat gcc tgc agt ggg gac agt gga gga cct tta gtg	2930
Lys Gly Arg Tyr Asp Ala Cys Ser Gly Asp Ser Gly Gly Pro Leu Val	
960 965 970	

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ttt gct gat gat tcc cgt acc gaa agg cgg tgg gtc ttg gaa ggg att 2978
 Phe Ala Asp Asp Ser Arg Thr Glu Arg Arg Trp Val Leu Glu Gly Ile
 975 980 985

gtc agc tgg ggc agt ccc agt gga tgt ggc aag gcg aac cag tac ggg 3026
 Val Ser Trp Gly Ser Pro Ser Gly Cys Gly Lys Ala Asn Gln Tyr Gly
 990 995 1000

ggc ttc act aaa gtt aac gtt ttc ctg tca tgg att agg cag ttc att 3074
 Gly Phe Thr Lys Val Asn Val Phe Leu Ser Trp Ile Arg Gln Phe Ile
 1005 1010 1015

tgaaactgat ctaaataattt taagcatggt tataaacgtc ttgtttccta ttattgcttt 3134

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tttttacaaa tggttatttt agtcagtga tgaagaatagt atccattgaa gactgttacc 3254

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ttctgtcatt ttaccataaa tttggtttct ggtgtgtgct aagtccacca gtagagaacg 3374

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<212> PRT

<213> Carcinoscorpius rotundicauda

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Cys Asp Glu Thr Arg Phe Glu Cys Lys Cys Gly Asp Pro Gly Tyr Val
 35 40 45

Phe Asn Ile Pro Val Lys Gln Cys Thr Tyr Phe Tyr Arg Trp Arg Pro
 50 55 60

Tyr Cys Lys Pro Cys Asp Asp Leu Glu Ala Lys Asp Ile Cys Pro Lys
 65 70 75 80

Tyr Lys Arg Cys Gln Glu Cys Lys Ala Gly Leu Asp Ser Cys Val Thr
 85 90 95

Cys Pro Pro Asn Lys Tyr Gly Thr Trp Cys Ser Gly Glu Cys Gln Cys
 100 105 110

Lys Asn Gly Gly Ile Cys Asp Gln Arg Thr Gly Ala Cys Ala Cys Arg
 115 120 125

Asp Arg Tyr Glu Gly Val His Cys Glu Ile Leu Lys Gly Cys Pro Leu
 130 135 140

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Leu Pro Ser Asp Ser Gln Val Gln Glu Val Arg Asn Pro Pro Asp Asn
 145 150 155 160
 Pro Gln Thr Ile Asp Tyr Ser Cys Ser Pro Gly Phe Lys Leu Lys Gly
 165 170 175
 Met Ala Arg Ile Ser Cys Leu Pro Asn Gly Gln Trp Ser Asn Phe Pro
 180 185 190
 Pro Lys Cys Ile Arg Glu Cys Ala Met Val Ser Ser Pro Glu His Gly
 195 200 205
 Lys Val Asn Ala Leu Ser Gly Asp Met Ile Glu Gly Ala Thr Leu Arg
 210 215 220
 Phe Ser Cys Asp Ser Pro Tyr Tyr Leu Ile Gly Gln Glu Thr Leu Thr
 225 230 235 240
 Cys Gln Gly Asn Gly Gln Trp Asn Gly Gln Ile Pro Gln Cys Lys Asn
 245 250 255
 Leu Val Phe Cys Pro Asp Leu Asp Pro Val Asn His Ala Glu His Lys
 260 265 270
 Val Lys Ile Gly Val Glu Gln Lys Tyr Gly Gln Phe Pro Gln Gly Thr
 275 280 285
 Glu Val Thr Tyr Thr Cys Ser Gly Asn Tyr Phe Leu Met Gly Phe Asp
 290 295 300
 Thr Leu Lys Cys Asn Pro Asp Gly Ser Trp Ser Gly Ser Gln Pro Ser
 305 310 315 320
 Cys Val Lys Val Ala Asp Arg Glu Val Asp Cys Asp Ser Lys Ala Val
 325 330 335
 Asp Phe Leu Asp Asp Val Gly Glu Pro Val Arg Ile His Cys Pro Ala
 340 345 350
 Gly Cys Ser Leu Thr Ala Gly Thr Val Trp Gly Thr Ala Ile Tyr His
 355 360 365
 Glu Leu Ser Ser Val Cys Arg Ala Ala Ile His Ala Gly Lys Leu Pro
 370 375 380
 Asn Ser Gly Gly Ala Val His Val Val Asn Asn Gly Pro Tyr Ser Asp
 385 390 395 400
 Phe Leu Gly Ser Asp Leu Asn Gly Ile Lys Ser Glu Glu Leu Lys Ser
 405 410 415
 Leu Ala Arg Ser Phe Arg Phe Asp Tyr Val Arg Ser Ser Thr Ala Gly
 420 425 430
 Lys Ser Gly Cys Pro Asp Gly Trp Phe Glu Val Asp Glu Asn Cys Val
 435 440 445
 Tyr Val Thr Ser Lys Gln Arg Ala Trp Glu Arg Ala Gln Gly Val Cys
 450 455 460

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Thr Asn Met Ala Ala Arg Leu Ala Val Leu Asp Lys Asp Val Ile Pro
 465 470 475 480
 Asn Ser Leu Thr Glu Thr Leu Arg Gly Lys Gly Leu Thr Thr Thr Trp
 485 490 495
 Ile Gly Leu His Arg Leu Asp Ala Glu Lys Pro Phe Ile Trp Glu Leu
 500 505 510
 Met Asp Arg Ser Asn Val Val Leu Asn Asp Asn Leu Thr Phe Trp Ala
 515 520 525
 Ser Gly Glu Pro Gly Asn Glu Thr Asn Cys Val Tyr Met Asp Ile Gln
 530 535 540
 Asp Gln Leu Gln Ser Val Trp Lys Thr Lys Ser Cys Phe Gln Pro Ser
 545 550 555 560
 Ser Phe Ala Cys Met Met Asp Leu Ser Asp Arg Asn Lys Ala Lys Cys
 565 570 575
 Asp Asp Pro Gly Ser Leu Glu Asn Gly His Ala Thr Leu His Gly Gln
 580 585 590
 Ser Ile Asp Gly Phe Tyr Ala Gly Ser Ser Ile Arg Tyr Ser Cys Glu
 595 600 605
 Val Leu His Tyr Leu Ser Gly Thr Glu Thr Val Thr Cys Thr Thr Asn
 610 615 620
 Gly Thr Trp Ser Ala Pro Lys Pro Arg Cys Ile Lys Val Ile Thr Cys
 625 630 635 640
 Gln Asn Pro Pro Val Pro Ser Tyr Gly Ser Val Glu Ile Lys Pro Pro
 645 650 655
 Ser Arg Thr Asn Ser Ile Ser Arg Val Gly Ser Pro Phe Leu Arg Leu
 660 665 670
 Pro Arg Leu Pro Leu Pro Leu Ala Arg Ala Ala Lys Pro Pro Pro Lys
 675 680 685
 Pro Arg Ser Ser Gln Pro Ser Thr Val Asp Leu Ala Ser Lys Val Lys
 690 695 700
 Leu Pro Glu Gly His Tyr Arg Val Gly Ser Arg Ala Ile Tyr Thr Cys
 705 710 715 720
 Glu Ser Arg Tyr Tyr Glu Leu Leu Gly Ser Gln Gly Arg Arg Cys Asp
 725 730 735
 Ser Asn Gly Asn Trp Ser Gly Arg Pro Ala Ser Cys Ile Pro Val Cys
 740 745 750
 Gly Arg Ser Asp Ser Pro Arg Ser Pro Phe Ile Trp Asn Gly Asn Ser
 755 760 765
 Thr Glu Ile Gly Gln Trp Pro Trp Gln Ala Gly Ile Ser Arg Trp Leu
 770 775 780

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Ala Asp His Asn Met Trp Phe Leu Gln Cys Gly Gly Ser Leu Leu Asn
785 790 795 800

Glu Lys Trp Ile Val Thr Ala Ala His Cys Val Thr Tyr Ser Ala Thr
805 810 815

Ala Glu Ile Ile Asp Pro Asn Gln Phe Lys Met Tyr Leu Gly Lys Tyr
820 825 830

Tyr Arg Asp Asp Ser Arg Asp Asp Asp Tyr Val Gln Val Arg Glu Ala
835 840 845

Leu Glu Ile His Val Asn Pro Asn Tyr Asp Pro Gly Asn Leu Asn Phe
850 855 860

Asp Ile Ala Leu Ile Gln Leu Lys Thr Pro Val Thr Leu Thr Thr Arg
865 870 875 880

Val Gln Pro Ile Cys Leu Pro Thr Asp Ile Thr Thr Arg Glu His Leu
885 890 895

Lys Glu Gly Thr Leu Ala Val Val Thr Gly Trp Gly Leu Asn Glu Asn
900 905 910

Asn Thr Tyr Ser Glu Thr Ile Gln Gln Ala Val Leu Pro Val Val Ala
915 920 925

Ala Ser Thr Cys Glu Glu Gly Tyr Lys Glu Ala Asp Leu Pro Leu Thr
930 935 940

Val Thr Glu Asn Met Phe Cys Ala Gly Tyr Lys Lys Gly Arg Tyr Asp
945 950 955 960

Ala Cys Ser Gly Asp Ser Gly Gly Pro Leu Val Phe Ala Asp Asp Ser
965 970 975

Arg Thr Glu Arg Arg Trp Val Leu Glu Gly Ile Val Ser Trp Gly Ser
980 985 990

Pro Ser Gly Cys Gly Lys Ala Asn Gln Tyr Gly Gly Phe Thr Lys Val
995 1000 1005

Asn Val Phe Leu Ser Trp Ile Arg Gln Phe Ile
1010 1015

<210> 7

<211> 36

<212> PRT

<213> Artificial Sequence

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<223> rS3-1mer

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1 5 10 15

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Gln Phe Pro Gln Gly Thr Glu Val Thr Tyr Thr Cys Ser Gly Asn Tyr
 20 25 30

Phe Leu Met Asp
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<210> 8

<211> 468

<212> DNA

<213> Artificial Sequence

<220>

<223> rS3-4mer

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 1 5 10 15

aaa tat ggt cag ttt cct caa ggc act gaa gtg acc tat acg tgt tcg 96
 Lys Tyr Gly Gln Phe Pro Gln Gly Thr Glu Val Thr Tyr Thr Cys Ser
 20 25 30

ggt aac tac ttc ttg atg gac ccc cag gat ccc cat gct gaa cac aag 144
 Gly Asn Tyr Phe Leu Met Asp Pro Gln Asp Pro His Ala Glu His Lys
 35 40 45

gtt aaa att ggt gtg gaa caa aaa tat ggt cag ttt cct caa ggc act 192
 Val Lys Ile Gly Val Glu Gln Lys Tyr Gly Gln Phe Pro Gln Gly Thr
 50 55 60

gaa gtg acc tat acg tgt tcg ggt aac tac ttc ttg atg gac ccc cag 240
 Glu Val Thr Tyr Thr Cys Ser Gly Asn Tyr Phe Leu Met Asp Pro Gln
 65 70 75 80

gat ccc cat gct gaa cac aag gtt aaa att ggt gtg gaa caa aaa tat 288
 Asp Pro His Ala Glu His Lys Val Lys Ile Gly Val Glu Gln Lys Tyr
 85 90 95

ggt cag ttt cct caa ggc act gaa gtg acc tat acg tgt tcg ggt aac 336
 Gly Gln Phe Pro Gln Gly Thr Glu Val Thr Tyr Thr Cys Ser Gly Asn
 100 105 110

tac ttc ttg atg gac ccc cag gat ccc cat gct gaa cac aag gtt aaa 384
 Tyr Phe Leu Met Asp Pro Gln Asp Pro His Ala Glu His Lys Val Lys
 115 120 125

att ggt gtg gaa caa aaa tat ggt cag ttt cct caa ggc act gaa gtg 432
 Ile Gly Val Glu Gln Lys Tyr Gly Gln Phe Pro Gln Gly Thr Glu Val
 130 135 140

acc tat acg tgt tcg ggt aac tac ttc ttg atg gac 468
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 145 150 155

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<210> 9

<211> 156

<212> PRT

<213> Artificial Sequence

<220>

<223> rS3-4mer

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20 25 30

Gly Asn Tyr Phe Leu Met Asp Pro Gln Asp Pro His Ala Glu His Lys
35 40 45

Val Lys Ile Gly Val Glu Gln Lys Tyr Gly Gln Phe Pro Gln Gly Thr
50 55 60

Glu Val Thr Tyr Thr Cys Ser Gly Asn Tyr Phe Leu Met Asp Pro Gln
65 70 75 80

Asp Pro His Ala Glu His Lys Val Lys Ile Gly Val Glu Gln Lys Tyr
85 90 95

Gly Gln Phe Pro Gln Gly Thr Glu Val Thr Tyr Thr Cys Ser Gly Asn
100 105 110

Tyr Phe Leu Met Asp Pro Gln Asp Pro His Ala Glu His Lys Val Lys
115 120 125

Ile Gly Val Glu Gln Lys Tyr Gly Gln Phe Pro Gln Gly Thr Glu Val
130 135 140

Thr Tyr Thr Cys Ser Gly Asn Tyr Phe Leu Met Asp
145 150 155